

SEQUENCE LISTING

<110> Sato, Aaron K.
Edge, Albert

<120> SERUM PROTEIN-ASSOCIATED TARGET-SPECIFIC
LIGANDS AND IDENTIFICATION METHOD THEREFOR

<130> 10280-058001

<150> US 60/390,657

<151> 2002-06-21

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 1

Ala	Gly	Pro	Thr	Trp	Cys	Glu	Asp	Asp	Trp	Tyr	Tyr	Cys	Trp	Leu	Phe
1				5					10					15	
Gly	Thr	Gly	Gly	Gly	Lys										
				20											

<210> 2

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 2

Gly	Asp	Ser	Arg	Val	Cys	Trp	Glu	Asp	Ser	Trp	Gly	Gly	Glu	Val	Cys
1				5					10					15	
Phe	Arg	Tyr	Asp	Pro	Gly	Gly	Gly	Lys							
				20				25							

<210> 3

<211> 585

<212> PRT

<213> Homo sapiens

<400> 3

Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu
1				5					10					15	
Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln
				20				25					30		

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80
 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125
 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140
 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr

				485					490					495			
Tyr	Val	Pro	Lys	Glu	Phe	Asn	Ala	Glu	Thr	Phe	Thr	Phe	His	Ala	Asp		
			500					505					510				
Ile	Cys	Thr	Leu	Ser	Glu	Lys	Glu	Arg	Gln	Ile	Lys	Lys	Gln	Thr	Ala		
		515					520					525					
Leu	Val	Glu	Leu	Val	Lys	His	Lys	Pro	Lys	Ala	Thr	Lys	Glu	Gln	Leu		
	530					535					540						
Lys	Ala	Val	Met	Asp	Asp	Phe	Ala	Ala	Phe	Val	Glu	Lys	Cys	Cys	Lys		
545				550						555					560		
Ala	Asp	Asp	Lys	Glu	Thr	Cys	Phe	Ala	Glu	Glu	Gly	Lys	Lys	Leu	Val		
			565						570					575			
Ala	Ala	Ser	Gln	Ala	Ala	Leu	Gly	Leu									
			580					585									

<210> 4

<211> 608

<212> PRT

<213> Mus musculus

<400> 4

Met	Lys	Trp	Val	Thr	Phe	Leu	Leu	Leu	Leu	Phe	Val	Ser	Gly	Ser	Ala		
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Phe	Ser	Arg	Gly	Val	Phe	Arg	Arg	Glu	Ala	His	Lys	Ser	Glu	Ile	Ala		
		20						25					30				
His	Arg	Tyr	Asn	Asp	Leu	Gly	Glu	Gln	His	Phe	Lys	Gly	Leu	Val	Leu		
		35				40						45					
Ile	Ala	Phe	Ser	Gln	Tyr	Leu	Gln	Lys	Cys	Ser	Tyr	Asp	Glu	His	Ala		
	50				55						60						
Lys	Leu	Val	Gln	Glu	Val	Thr	Asp	Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp		
65				70					75					80			
Glu	Ser	Ala	Ala	Asn	Cys	Asp	Lys	Ser	Leu	His	Thr	Leu	Phe	Gly	Asp		
			85					90						95			
Lys	Leu	Cys	Ala	Ile	Pro	Asn	Leu	Arg	Glu	Asn	Tyr	Gly	Glu	Leu	Ala		
		100					105						110				
Asp	Cys	Cys	Thr	Lys	Gln	Glu	Pro	Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln		
		115				120						125					
His	Lys	Asp	Asp	Asn	Pro	Ser	Leu	Pro	Pro	Phe	Glu	Arg	Pro	Glu	Ala		
	130					135					140						
Glu	Ala	Met	Cys	Thr	Ser	Phe	Lys	Glu	Asn	Pro	Thr	Thr	Phe	Met	Gly		
145				150					155						160		
His	Tyr	Leu	His	Glu	Val	Ala	Arg	Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro		
			165						170					175			
Glu	Leu	Leu	Tyr	Tyr	Ala	Glu	Gln	Tyr	Asn	Glu	Ile	Leu	Thr	Gln	Cys		
		180						185					190				
Cys	Ala	Glu	Ala	Asp	Lys	Glu	Ser	Cys	Leu	Thr	Pro	Lys	Leu	Asp	Gly		
		195				200						205					
Val	Lys	Glu	Lys	Ala	Leu	Val	Ser	Ser	Val	Arg	Gln	Arg	Met	Lys	Cys		
	210					215						220					
Ser	Ser	Met	Gln	Lys	Phe	Gly	Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val		
225				230						235				240			
Ala	Arg	Leu	Ser	Gln	Thr	Phe	Pro	Asn	Ala	Asp	Phe	Ala	Glu	Ile	Thr		
			245						250					255			
Lys	Leu	Ala	Thr	Asp	Leu	Thr	Lys	Val	Asn	Lys	Glu	Cys	Cys	His	Gly		
		260						265					270				
Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	Arg	Ala	Glu	Leu	Ala	Lys	Tyr	Met		
		275					280					285					
Cys	Glu	Asn	Gln	Ala	Thr	Ile	Ser	Ser	Lys	Leu	Gln	Thr	Cys	Cys	Asp		

290		295		300
Lys Pro Leu Leu Lys Lys	Ala His Cys Leu Ser	Glu Val Glu His Asp		
305		310		315
Thr Met Pro Ala Asp	Leu Pro Ala Ile Ala Ala	Asp Phe Val Glu Asp		320
	325		330	335
Gln Glu Val Cys Lys Asn Tyr Ala	Glu Ala Lys Asp Val Phe Leu Gly			
	340		345	350
Thr Phe Leu Tyr Glu Tyr Ser Arg	Arg His Pro Asp Tyr Ser Val Ser			
	355		360	365
Leu Leu Leu Arg Leu Ala Lys Lys Tyr Glu Ala	Thr Leu Glu Lys Cys			
	370		375	380
Cys Ala Glu Ala Asn Pro Pro Ala Cys Tyr Gly Thr	Val Leu Ala Glu			
385		390		395
Phe Gln Pro Leu Val Glu Glu Pro Lys Asn Leu Val Lys Thr	Asn Cys			
	405		410	415
Asp Leu Tyr Glu Lys Leu Gly Glu Tyr Gly Phe Gln Asn Ala Ile Leu				
	420		425	430
Val Arg Tyr Thr Gln Lys Ala Pro Gln Val Ser Thr Pro Thr Leu Val				
	435		440	445
Glu Ala Ala Arg Asn Leu Gly Arg Val Gly Thr Lys Cys Cys Thr Leu				
	450		455	460
Pro Glu Asp Gln Arg Leu Pro Cys Val Glu Asp Tyr Leu Ser Ala Ile				
465		470		475
Leu Asn Arg Val Cys Leu Leu His Glu Lys Thr Pro Val Ser Glu His				
	485		490	495
Val Thr Lys Cys Cys Ser Gly Ser Leu Val Glu Arg Arg Pro Cys Phe				
	500		505	510
Ser Ala Leu Thr Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Lys Ala				
	515		520	525
Glu Thr Phe Thr Phe His Ser Asp Ile Cys Thr Leu Pro Glu Lys Glu				
	530		535	540
Lys Gln Ile Lys Lys Gln Thr Ala Leu Ala Glu Leu Val Lys His Lys				
545		550		555
Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp Phe Ala				
	565		570	575
Gln Phe Leu Asp Thr Cys Cys Lys Ala Ala Asp Lys Asp Thr Cys Phe				
	580		585	590
Ser Thr Glu Gly Pro Asn Leu Val Thr Arg Cys Lys Asp Ala Leu Ala				
	595		600	605

<210> 5

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> template sequence

<221> VARIANT

<222> 1-3, 5-8, 10-12

<223> Xaa = any common alfa-amino acids, except
cysteine (Cys)

<400> 5

Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa

1

5

10

<210> 6
 <211> 13
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 <213> Artificial Sequence

<220>
 <223> template sequence

<221> VARIANT
 <222> 1-3, 5-9, 11-13
 <223> Xaa = any common alfa-amino acids, except cysteine
 (Cys)

<400> 6
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10

<210> 7
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> template sequence

<221> VARIANT
 <222> 1-3, 5-10, 12-14
 <223> Xaa = any amino acid except cysteine (Cys)

<400> 7
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10

<210> 8
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> template sequence

<221> VARIANT
 <222> 1-3, 5-11, 13-15
 <223> Xaa = any amino acid except cysteine (Cys)

<400> 8
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
 1 5 10 15

<210> 9
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 <213> Artificial Sequence

<220>
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